

SCORE Search Results Details for Application 10526521 and Search Result 20070808_155054_us-10-526-521a-15.rng.

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This page gives you Search Results detail for the Application 10526521 and Search Result 20070808_155054_us-10-526-521a-15.rng.

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GenCore version 6.2.1
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OM nucleic - nucleic search, using sw model

Run on: August 9, 2007, 18:15:57 ; Search time 357 Seconds
(without alignments)
269.853 Million cell updates/sec

Title: US-10-526-521A-15
Perfect score: 13
Sequence: 1 tggtgagtcacca 13

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : N_Geneseq_200701:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

16: geneseqn2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No. | Score | % Query Match | Length | DB | ID | Description |
|--------|-----|-------|---------------------|--------|----|----------|--------------------|
| c | 1 | 13 | 100.0 | 13 | 12 | ADO57900 | Ado57900 Transcrip |
| | 2 | 13 | 100.0 | 13 | 12 | ADO57879 | Ado57879 Transcrip |
| | 3 | 13 | 100.0 | 15 | 12 | ADO57904 | Ado57904 Transcrip |
| c | 4 | 13 | 100.0 | 15 | 12 | ADO57899 | Ado57899 Transcrip |
| | 5 | 13 | 100.0 | 15 | 12 | ADO57880 | Ado57880 Transcrip |
| c | 6 | 13 | 100.0 | 15 | 12 | ADO57875 | Ado57875 Transcrip |
| | 7 | 13 | 100.0 | 17 | 12 | ADO57903 | Ado57903 Transcrip |
| c | 8 | 13 | 100.0 | 17 | 12 | ADO57876 | Ado57876 Transcrip |
| c | 9 | 13 | 100.0 | 17 | 12 | ADO57898 | Ado57898 Transcrip |
| | 10 | 13 | 100.0 | 17 | 12 | ADO57881 | Ado57881 Transcrip |
| c | 11 | 13 | 100.0 | 19 | 12 | ADO57897 | Ado57897 Transcrip |
| | 12 | 13 | 100.0 | 19 | 12 | ADO57882 | Ado57882 Transcrip |
| c | 13 | 13 | 100.0 | 19 | 12 | ADQ36695 | Adq36695 Primer 3 |
| c | 14 | 13 | 100.0 | 21 | 12 | ADO57896 | Ado57896 Transcrip |
| | 15 | 13 | 100.0 | 21 | 12 | ADO57883 | Ado57883 Transcrip |
| c | 16 | 13 | 100.0 | 116 | 12 | ACH89045 | Ach89045 Human gen |
| c | 17 | 13 | 100.0 | 231 | 4 | AAL21284 | Aal21284 Human bre |
| | 18 | 13 | 100.0 | 250 | 14 | AEH10788 | Aeh10788 RAS homol |

```

<!--StartFragment-->RESULT 17
AAL21284/c
ID   AAL21284 standard; cDNA; 231 BP.
XX
AC   AAL21284;
XX
DT   07-DEC-2001   (first entry)
XX
DE   Human breast cancer expressed polynucleotide 13741.
XX
KW   Human; breast cancer; cell marker; cytostatic; ss.
XX
OS   Homo sapiens.
XX
PN   WO200151628-A2.
XX
PD   19-JUL-2001.
XX
PF   10-JAN-2001; 2001WO-US000798.
XX
PR   14-JAN-2000; 2000US-0176077P.
PR   14-MAR-2000; 2000US-0189167P.
PR   24-MAR-2000; 2000US-0192099P.
PR   29-MAR-2000; 2000US-0193480P.
PR   15-MAY-2000; 2000US-0205230P.
PR   09-JUN-2000; 2000US-0211315P.
PR   25-JUL-2000; 2000US-0220534P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Lillie J, Xu Y, Wang Y, Steinmann K;
XX
DR   WPI; 2001-451856/48.
XX
PT   New peptide useful as a marker for the diagnosis of breast cancer.
XX
PS   Claim 1; Page 2444; 3695pp; English.
XX
CC   The invention relates to human breast cancer expressed polynucleotides
CC   (AAL07544-AAL26789) and methods of assessing whether a patient is
CC   afflicted with breast cancer by examining the correlation between the
CC   expression of certain markers and the cancerous state of breast cells.
CC   The polynucleotides and encoded polypeptides are potential markers for
CC   detecting, diagnosing, monitoring, characterising treating and
CC   potentially preventing breast cancer. The polynucleotides and encoded
CC   polypeptides are also useful for isolating compounds with cytostatic
CC   activity
XX
SQ   Sequence 231 BP; 62 A; 67 C; 49 G; 53 T; 0 U; 0 Other;

Query Match          100.0%; Score 13; DB 4; Length 231;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TGGTGAGTCACCA 13
        |||||
Db      25 TGGTGAGTCACCA 13

```

<!--EndFragment-->